

UID: SEQ ID NO:38 Type: DNA 1267 bp
SEQ ID NO:38

vs.

UID: Jacobs et. al. Type: DNA 481 bp
Jacobs et. al.

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Local similarity
Match: 19
Mismatch: -17
Indel start: -13
Indel extend: -7
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Score: 8776 at (SEQ ID NO:38) [456..951] : (Jacobs et. al.) [1..481]

Arrow indicates polynucleotide encoding the C-terminal 15 amino acids of SEQ ID NO:83.

TGA = STOP codon for SEQ ID NO:83

512 CAACGGGATTCTTGCTTGTAAAATGTTGCAGTCCACCTGTCCAACTTGATCTTCCGGA
50 CAACGGGATTCTTGCTTGTAAAATGTTGCAGTCCACCTGTCCAACTTGATCTTCCGGA

572 CATTTGACTTGTTCCTGGTTATCCACCATCTCTTGCCCTTCTGGGTTCTGGCTGCT
|||||||
110 CATTTGACTTGTTCCTGGTTATCCACCATCTCTTGCCCTTCTGGGTTCTGGCTGCT

632 TGGTCAATCTCAAGCTGGCCACTATCTAGCTATGACCACGTTGCTCTGGAGATGAGCA
|||||||
170 TGGTCAATCTCAAGCTGGCCACTATCTAGCTATGACCACGTTGCTCTGGAGATGAGCA

752 GGAAGCTCAACCACTGGCTGATGATTCACATGTTCACTGCCGATGGTCTAACCTACCC
|||||
290 GGAAGCTCAACCACTGGCTGATGATTCACATGTTCACTGCCGATGGTCTAACCTACCC

812 ACATGTGGTGGGTGTGTTCTGGCACTGGGACGGCCTGGTCAGCAGCCTGTATCTGCCTC
350 ACATGTGGTGGGTGTGTTCTGGCACTGGGACGGCCTGGTCAGCAGCCTGTATCTGCCTC

872 ATTTGACACTGTTCTTGTGGACTGGCTCTGCTTACGCTAACATTAAATCCATATTGGA
410 ATTTGACACTGTTCTTGTGGACTGGCTCTGCTTACGCTAACATTAAATCCATATTGGA

932 CCCATAAGAAGACTCAGCAG
 ||| ||||||| | |||
 470 CCC-----AGACTC-G-AG

Percent Identity: 95.0
Percent Similarity: 95.0